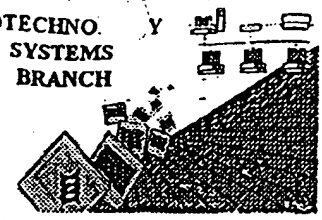
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/817,431
Source: TWO
Date Processed by STIC: 4/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/817,431

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING DATE: 04/08/2004
PATENT APPLICATION: **US/10/817,431** TIME: 16:14:49

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF4\04082004\J817431.raw**

```
      4 <110> APPLICANT: Degussa AG
      7 <120> TITLE OF INVENTION: Process for the production of L-amino acids using strains of
the
      8       Enterobacteriaceae family
     11 <130> FILE REFERENCE: 020489 BT
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/817,431
C--> 14 <141> CURRENT FILING DATE: 2004-04-05
     14 <160> NUMBER OF SEQ ID NOS: 8
     17 <170> SOFTWARE: PatentIn version 3.1
     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 30
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Synthetic sequence
     26 <220> FEATURE:
W--> 27 <221> NAME/KEY: Primer
     28 <222> LOCATION: (1)..(30)
     29 <223> OTHER INFORMATION: yfiD1
     32 <220> FEATURE:
W--> 33 <221> NAME/KEY: Restriction site
     34 <222> LOCATION: (9)..(14)
     35 <223> OTHER INFORMATION: XbaI site
     38 <400> SEQUENCE: 1
     39 gaacaaatct agaaattaag ccggggaggc
     41 <210> SEQ ID NO: 2
     42 <211> LENGTH: 24
     43 <212> TYPE: DNA
     44 <213> ORGANISM: Synthetic sequence
     47 <220> FEATURE:
W--> 48 <221> NAME/KEY: Primer
     49 <222> LOCATION: (1)..(24)
     50 <223> OTHER INFORMATION: yfiD2
     53 <220> FEATURE:
W--> 54 <221> NAME/KEY: Restriction site
     55 <222> LOCATION: (8)..(13)
     56 <223> OTHER INFORMATION: HindIII site
     59 <400> SEQUENCE: 2
     60 gctacttaag ctttacaggc tttc                                          24
     62 <210> SEQ ID NO: 3
     64 <211> LENGTH: 431
     65 <212> TYPE: DNA
     66 <213> ORGANISM: Escherichia coli
     69 <220> FEATURE:
W--> 70 <221> NAME/KEY: yfiD PCR product
     71 <222> LOCATION: (1)..(431)
```

Does Not Comply
Corrected Diskette Needed

(Pg. 1

-Invalid Response

mandatory <213> Response has to be either Artificial Unknown or Genus/Species,

Please see item # 10 on error summary sheet.

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04082004\J817431.raw

```
 72 <223> OTHER INFORMATION:
 75 <220> FEATURE:
 76 <221> NAME/KEY: CDS
 77 <222> LOCATION: (36)..(419)
 78 <223> OTHER INFORMATION: open reading frame yfiD
W--> 81 <400> 3
 82 gaacaaatct agaaattaag ccggggaggc atcac atg att aca ggt atc cag        53
 83                                       Met Ile Thr Gly Ile Gln
 84                                       1               5
 86 att act aaa gcc gct aac gac gat ctg ctg aac tct ttc tgg ctg ctg       101
 87 Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu Asn Ser Phe Trp Leu Leu
 88             10                  15                  20
 90 gac agc gaa aaa ggc gaa gcg cgt tgc atc gtt gca aaa gca ggt tat       149
 91 Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile Val Ala Lys Ala Gly Tyr
 92         25                  30                  35
 94 gca gaa gat gaa gtg gtt gca gta agc aaa ctg ggt gac att gaa tac       197
 95 Ala Glu Asp Glu Val Val Ala Val Ser Lys Leu Gly Asp Ile Glu Tyr
 96     40                  45                  50
 98 cgt gaa gtt cca gta gaa gtg aaa cca gaa gtt cgc gtt gaa ggt ggt       245
 99 Arg Glu Val Pro Val Glu Val Lys Pro Glu Val Arg Val Glu Gly Gly
100 55                  60                  65                  70
102 caa cac ctg aac gtt aac gtt ctg cgt cgc gaa act ctg gaa gat gca       293
103 Gln His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Glu Asp Ala
104                 75                  80                  85
106 gtt aag cat ccg gaa aaa tat ccg cag ctg acc atc cgt gta tcc ggt       341
107 Val Lys His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly
108             90                  95                  100
110 tat gca gtt cgc ttt aac tct ctg act ccg gaa cag cag cgc gac gtt       389
111 Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val
112         105                 110                 115
114 atc gct cgt acc ttt act gaa agc ctg taa agcttaagta gc                431
115 Ile Ala Arg Thr Phe Thr Glu Ser Leu
116     120                 125
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 127
121 <212> TYPE: PRT
122 <213> ORGANISM: Escherichia coli
125 <400> SEQUENCE: 4
126 Met Ile Thr Gly Ile Gln Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu
127 1               5                   10                  15
129 Asn Ser Phe Trp Leu Leu Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile
130             20                  25                  30
132 Val Ala Lys Ala Gly Tyr Ala Glu Asp Glu Val Val Ala Val Ser Lys
133         35                  40                  45
135 Leu Gly Asp Ile Glu Tyr Arg Glu Val Pro Val Glu Val Lys Pro Glu
136     50                  55                  60
138 Val Arg Val Glu Gly Gly Gln His Leu Asn Val Asn Val Leu Arg Arg
139 65                  70                  75                  80
141 Glu Thr Leu Glu Asp Ala Val Lys His Pro Glu Lys Tyr Pro Gln Leu
```

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04082004\J817431.raw

```
142                 85                  90                  95
144 Thr Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro
145             100                 105                 110
147 Glu Gln Gln Arg Asp Val Ile Ala Arg Thr Phe Thr Glu Ser Leu
148         115                 120                 125
150 <210> SEQ ID NO: 5
151 <211> LENGTH: 28
152 <212> TYPE: DNA
153 <213> ORGANISM: Synthetic sequence
156 <220> FEATURE:
W--> 157 <221> NAME/KEY: Primer
158 <222> LOCATION: (1)..(28)
159 <223> OTHER INFORMATION: pflB1
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: Restriction site
164 <222> LOCATION: (5)..(10)
165 <223> OTHER INFORMATION: XbaI site
168 <400> SEQUENCE: 5
169 ccactctaga aggtaggtgt tacatgtc                                    28
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Synthetic sequence
177 <220> FEATURE:
W--> 178 <221> NAME/KEY: Primer
179 <222> LOCATION: (1)..(27)
180 <223> OTHER INFORMATION: pflB2
183 <220> FEATURE:
W--> 184 <221> NAME/KEY: Restriction site
185 <222> LOCATION: (13)..(18)
186 <223> OTHER INFORMATION: HindIII site
189 <400> SEQUENCE: 6
190 cgatttcagt caaagcttat tacatag                                     27
193 <210> SEQ ID NO: 7
194 <211> LENGTH: 2325
195 <212> TYPE: DNA
196 <213> ORGANISM: Escherichia coli
199 <220> FEATURE:
W--> 200 <221> NAME/KEY: pflB PCR product
201 <222> LOCATION: (1)..(2325)
202 <223> OTHER INFORMATION:
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (24)..(2306)
208 <223> OTHER INFORMATION: pflB coding region
W--> 211 <400> 7
212 ccactctaga aggtaggtgt tac atg tcc gag ctt aat gaa aag tta gcc aca    53
213                         Met Ser Glu Leu Asn Glu Lys Leu Ala Thr
214                         1               5                   10
```

same error

same error

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04082004\J817431.raw

```
216 gcc tgg gaa ggt ttt acc aaa ggt gac tgg cag aat gaa gta aac gtc      101
217 Ala Trp Glu Gly Phe Thr Lys Gly Asp Trp Gln Asn Glu Val Asn Val
218                 15                  20                  25
220 cgt gac ttc att cag aaa aac tac act ccg tac gag ggt gac gag tcc      149
221 Arg Asp Phe Ile Gln Lys Asn Tyr Thr Pro Tyr Glu Gly Asp Glu Ser
222             30                  35                  40
224 ttc ctg gct ggc gct act gaa gcg acc acc acc ctg tgg gac aaa gta      197
225 Phe Leu Ala Gly Ala Thr Glu Ala Thr Thr Thr Leu Trp Asp Lys Val
226         45                  50                  55
228 atg gaa ggc gtt aaa ctg gaa aac cgc act cac gcg cca gtt gac ttt      245
229 Met Glu Gly Val Lys Leu Glu Asn Arg Thr His Ala Pro Val Asp Phe
230     60                  65                  70
232 gac acc gct gtt gct tcc acc atc acc tct cac gac gct ggc tac atc      293
233 Asp Thr Ala Val Ala Ser Thr Ile Thr Ser His Asp Ala Gly Tyr Ile
234 75                  80                  85                  90
236 aac aag cag ctt gag aaa atc gtt ggt ctg cag act gaa gct ccg ctg      341
237 Asn Lys Gln Leu Glu Lys Ile Val Gly Leu Gln Thr Glu Ala Pro Leu
238                 95                  100                 105
240 aaa cgt gct ctt atc ccg ttc ggt ggt atc aaa atg atc gaa ggt tcc      389
241 Lys Arg Ala Leu Ile Pro Phe Gly Gly Ile Lys Met Ile Glu Gly Ser
242             110                 115                 120
244 tgc aaa gcg tac aac cgc gaa ctg gat ccg atg atc aaa aaa atc ttc      437
245 Cys Lys Ala Tyr Asn Arg Glu Leu Asp Pro Met Ile Lys Lys Ile Phe
246         125                 130                 135
248 act gaa tac cgt aaa act cac aac cag ggc gtg ttc gac gtt tac act      485
249 Thr Glu Tyr Arg Lys Thr His Asn Gln Gly Val Phe Asp Val Tyr Thr
250     140                 145                 150
252 ccg gac atc ctg cgt tgc cgt aaa tct ggt gtt ctg acc ggt ctg cca      533
253 Pro Asp Ile Leu Arg Cys Arg Lys Ser Gly Val Leu Thr Gly Leu Pro
254 155                 160                 165                 170
256 gat gca tat ggc cgt ggc cgt atc atc ggt gac tac cgt cgc gtt gcg      581
257 Asp Ala Tyr Gly Arg Gly Arg Ile Ile Gly Asp Tyr Arg Arg Val Ala
258                 175                 180                 185
260 ctg tac ggt atc gac tac ctg atg aaa gac aaa ctg gca cag ttc act      629
261 Leu Tyr Gly Ile Asp Tyr Leu Met Lys Asp Lys Leu Ala Gln Phe Thr
262             190                 195                 200
264 tct ctg cag gct gat ctg gaa aac ggc gta aac ctg gaa cag act atc      677
265 Ser Leu Gln Ala Asp Leu Glu Asn Gly Val Asn Leu Glu Gln Thr Ile
266         205                 210                 215
268 cgt ctg cgc gaa gaa atc gct gaa cag cac cgc gct ctg ggt cag atg      725
269 Arg Leu Arg Glu Glu Ile Ala Glu Gln His Arg Ala Leu Gly Gln Met
270     220                 225                 230
272 aaa gaa atg gct gcg aaa tac ggc tac gac atc tct ggt ccg gct acc      773
273 Lys Glu Met Ala Ala Lys Tyr Gly Tyr Asp Ile Ser Gly Pro Ala Thr
274 235                 240                 245                 250
276 aac gct cag gaa gct atc cag tgg act tac ttc ggc tac ctg gct gct      821
277 Asn Ala Gln Glu Ala Ile Gln Trp Thr Tyr Phe Gly Tyr Leu Ala Ala
278                 255                 260                 265
280 gtt aag tct cag aac ggt gct gca atg tcc ttc ggt cgt acc tcc acc      869
```

RAW SEQUENCE LISTING DATE: 04/08/2004
PATENT APPLICATION: US/10/817,431 TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04082004\J817431.raw

```
281 Val Lys Ser Gln Asn Gly Ala Ala Met Ser Phe Gly Arg Thr Ser Thr
282             270                 275                 280
284 ttc ctg gat gtg tac atc gaa cgt gac ctg aaa gct ggc aag atc acc      917
285 Phe Leu Asp Val Tyr Ile Glu Arg Asp Leu Lys Ala Gly Lys Ile Thr
286         285                 290                 295
288 gaa caa gaa gcg cag gaa atg gtt gac cac ctg gtc atg aaa ctg cgt      965
289 Glu Gln Glu Ala Gln Glu Met Val Asp His Leu Val Met Lys Leu Arg
290     300                 305                 310
292 atg gtt cgc ttc ctg cgt act ccg gaa tac gat gaa ctg ttc tct ggc     1013
293 Met Val Arg Phe Leu Arg Thr Pro Glu Tyr Asp Glu Leu Phe Ser Gly
294 315                 320                 325                 330
296 gac ccg atc tgg gca acc gaa tct atc ggt ggt atg ggc ctc gac ggt     1061
297 Asp Pro Ile Trp Ala Thr Glu Ser Ile Gly Gly Met Gly Leu Asp Gly
298                 335                 340                 345
300 cgt acc ctg gtt acc aaa aac agc ttc cgt ttc ctg aac acc ctg tac     1109
301 Arg Thr Leu Val Thr Lys Asn Ser Phe Arg Phe Leu Asn Thr Leu Tyr
302             350                 355                 360
304 acc atg ggt ccg tct ccg gaa ccg aac atg acc att ctg tgg tct gaa     1157
305 Thr Met Gly Pro Ser Pro Glu Pro Asn Met Thr Ile Leu Trp Ser Glu
306         365                 370                 375
308 aaa ctg ccg ctg aac ttc aag aaa ttc gcc gct aaa gtg tcc atc gac     1205
309 Lys Leu Pro Leu Asn Phe Lys Lys Phe Ala Ala Lys Val Ser Ile Asp
310     380                 385                 390
312 acc tct tct ctg cag tat gag aac gat gac ctg atg cgt ccg gac ttc     1253
313 Thr Ser Ser Leu Gln Tyr Glu Asn Asp Asp Leu Met Arg Pro Asp Phe
314 395                 400                 405                 410
316 aac aac gat gac tac gct att gct tgc tgc gta agc ccg atg atc gtt     1301
317 Asn Asn Asp Asp Tyr Ala Ile Ala Cys Cys Val Ser Pro Met Ile Val
318                 415                 420                 425
320 ggt aaa caa atg cag ttc ttc ggt gcg cgt gca aac ctg gcg aaa acc     1349
321 Gly Lys Gln Met Gln Phe Phe Gly Ala Arg Ala Asn Leu Ala Lys Thr
322             430                 435                 440
324 atg ctg tac gca atc aac ggc ggc gtt gac gaa aaa ctg aaa atg cag     1397
325 Met Leu Tyr Ala Ile Asn Gly Gly Val Asp Glu Lys Leu Lys Met Gln
326         445                 450                 455
328 gtt ggt ccg aag tct gaa ccg atc aaa ggc gat gtc ctg aac tat gat     1445
329 Val Gly Pro Lys Ser Glu Pro Ile Lys Gly Asp Val Leu Asn Tyr Asp
330     460                 465                 470
332 gaa gtg atg gag cgc atg gat cac ttc atg gac tgg ctg gct aaa cag     1493
333 Glu Val Met Glu Arg Met Asp His Phe Met Asp Trp Leu Ala Lys Gln
334 475                 480                 485                 490
336 tac atc act gca ctg aac atc atc cac tac atg cac gac aag tac agc     1541
337 Tyr Ile Thr Ala Leu Asn Ile Ile His Tyr Met His Asp Lys Tyr Ser
338                 495                 500                 505
340 tac gaa gcc tct ctg atg gcg ctg cac gac cgt gac gtt atc cgc acc     1589
341 Tyr Glu Ala Ser Leu Met Ala Leu His Asp Arg Asp Val Ile Arg Thr
342             510                 515                 520
344 atg gcg tgt ggt atc gct ggt ctg tcc gtt gct gct gac tcc ctg tct     1637
345 Met Ala Cys Gly Ile Ala Gly Leu Ser Val Ala Ala Asp Ser Leu Ser
```

VERIFICATION SUMMARY DATE: 04/08/2004
PATENT APPLICATION: **US/10/817,431** TIME: 16:14:50

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF4\04082004\J817431.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:81 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:72
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:202